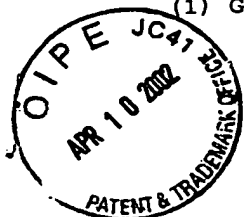


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SEQUENCE LISTING

APR 12 2002

TECH CENTER 1600/2900



(1) GENERAL INFORMATION:

- (i) APPLICANT: Jaye, Michael C.
Lynch, Kevin J.
Amin, Dilip V.
Doan, Kim-Anh T.
Marchadier, Dawn
Maugeais, Cyrille
Rader, Daniel J.
Krawiec, John A.
South, Victoria J.
- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EFFECTING THE LEVELS OF HIGH DENSITY LIPOPROTEIN (HDL) CHOLESTEROL AND APOLIPOPROTEIN AI, VERY LOW DENSITY LIPOPROTEIN (VLDL) CHOLESTEROL AND LOW DENSITY LIPOPROTEIN (LDL) CHOLESTEROL
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Synnestvedt & Lechner LLP
(B) STREET: Suite 2600 Aramark Tower, 1101 Market Street
(C) CITY: Philadelphia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19107
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-Windows 95
(D) SOFTWARE: Corel WordPerfect 8.0 converted to ASCII
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/277,401
(B) FILING DATE: March 26, 1999
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Kelly, Ph.D., Patrick J.
(B) REGISTRATION NUMBER: 34,638
(C) REFERENCE/DOCKET NUMBER: 22,944-C USA
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (215)923-4466
(B) TELEFAX: (215)923-2189

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 22..180
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | | | | | | | | |
|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| GAATTCGGCT | TGATCAATCG | C | TTC | AAA | AAG | GGG | ATC | TGT | CTG | AGC | TGC | CGC | 51 | | | |
| | | | Phe | Lys | Lys | Gly | Ile | Cys | Leu | Ser | Cys | Arg | | | | |
| | | | 1 | | | | 5 | | | | | 10 | | | | |
| AAG | AAC | CGT | TGT | AAT | AGC | ATT | GGC | TAC | AAT | GCC | AAG | AAA | ATG | AGG | AAC | 99 |
| Lys | Asn | Arg | Cys | Asn | Ser | Ile | Gly | Tyr | Asn | Ala | Lys | Lys | Met | Arg | Asn | |
| | | | 15 | | | | 20 | | | | | | 25 | | | |

AAG AGG AAC AGC AAA ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC	147
Lys Arg Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe	
30 35 40	
AGA GGT AAC CTT CAG TCC CTG GAG TGT CCC TGA GGAAGGCCCT TAATACCTCC	200
Arg Gly Asn Leu Gln Ser Leu Glu Cys Pro	
45 50	
TTCTTAATAC CATGCTGCAG AGCAGGGCAC ATCCTAGCCC AGGAGAAGTG GCCAGCACAA	260
TCCAATCAAAA TCGTTGCAAA TCAGATTACA CTGTGCATGT CCTAGGAAAG GGAATCTTTA	320
CAAAATAAAC AGTGTGGACC CCTCAAAAAA AAAAAAAGC CGAATTC	367

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg	Cys	Asn	Ser
1				5					10					15	
Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg	Asn	Ser	Lys	Met
			20					25					30		
Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg	Gly	Asn	Leu	Gln	Ser
		35					40						45		
Leu	Glu	Cys	Pro												
		50													

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 312..1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCT TCTACTACTA CTAGGCCACG CGTCGCCTAG TACGGGGGGG GGGGGGGGGG	60
TCAGCGAGTC CTGCGCTCCC GGCGGCTCAG GACGAGGGCA GATCTCGTTC TGGGGCAAGC	120
CGTTGACACT CGCTCCCTGC CACCGCCCGG GCTCCGTGCC GCCAAGTTTT CATTTTCCAC	180
CTTCTCTGCC TCCAGTCCCC CAGCCCCTGG CCGAGAGAAG GGTCTTACCG GCCGGGATTG	240
CTGGAAACAC CAAGAGGTGG TTTTGTGTTT TTAAACTTC TGTTTCTTGG GAGGGGGTGT	300
GGCGGGGCAG G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC	350
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu	
1 5 10	
TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA	398
Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly	
15 20 25	
CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC	446
Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val	
30 35 40 45	
AAA CCA TCT GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT	494
Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His	
50 55 60	
GAA GGA TGC TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC	542
Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys	
65 70 75	
AGT TTC AAC ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG	590
Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr	
80 85 90	

71
cont.

ATG AGC GGT ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG 638
 Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu
 95 100 105
 CAC ACA AGA GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC 686
 His Thr Arg Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro
 110 115 120 125
 CTG GCC CAC CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG 734
 Leu Ala His Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val
 130 135 140
 GGA CAC AGC ATT GCC AGG ATG CTC GAC TGG CTG CAG GAG AAG GAC GAT 782
 Gly His Ser Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp
 145 150 155
 TTT TCT CTC GGG AAT GTC CAC TTG ATC GGC TAC AGC CTC GGA GCG CAC 830
 Phe Ser Leu Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His
 160 165 170
 GTG GCC GGG TAT GCA GGC AAC TTC GTG AAA GGA ACG GTG GGC CGA ATC 878
 Val Ala Gly Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile
 175 180 185
 ACA GGT TTG GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC 926
 Thr Gly Leu Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His
 190 195 200 205
 AAG AGG CTC TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC 974
 Lys Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr
 210 215 220
 TAC ACG CGT TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC 1022
 Tyr Thr Arg Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly
 225 230 235
 CAC ATT GAC ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA 1070
 His Ile Asp Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly
 240 245 250
 CTC AAC GAT GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG 1118
 Leu Asn Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val
 255 260 265
 GTA AAA TGT GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG 1166
 Val Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu
 270 275 280 285
 GTG AAT CAG GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT 1214
 Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn
 290 295 300
 CGC TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT 1262
 Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn
 305 310 315
 AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA 1310
 Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys
 320 325 330
 ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC AGA GGT AAC CTT CAG 1358
 Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln
 335 340 345
 TCC CTG GAG TGT CAAGCCGAAT TC 1382
 Ser Leu Glu Cys
 350

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
 1 5 10 15

Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
 20 25 30
 Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
 35 40 45
 Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
 50 55 60
 Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
 65 70 75 80
 Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
 85 90 95
 Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
 100 105 110
 Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His
 115 120 125
 Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
 130 135 140
 Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
 145 150 155 160
 Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
 165 170 175
 Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
 180 185 190
 Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
 195 200 205
 Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
 210 215 220
 Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
 225 230 235 240
 Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
 245 250 255
 Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
 260 265 270
 Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
 275 280 285
 Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
 290 295 300
 Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
 305 310 315 320
 Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
 325 330 335
 Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
 340 345 350
 Cys

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC TGC TAT TGC
 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
 1 5 10 15

48

TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA CGG CTG GAA

96